



A DOCPHOENIX

## APPL PARTS

\_\_\_\_\_**IMIS**\_\_\_\_\_  
Internal Misc. Paper

\_\_\_\_\_**LET.**\_\_\_\_\_  
Misc. Incoming Letter

\_\_\_\_\_**371P**\_\_\_\_\_  
PCT Papers in a 371 Application

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Amendment Including Elections

\_\_\_\_\_**ABST**\_\_\_\_\_  
Abstract

\_\_\_\_\_**ADS**\_\_\_\_\_  
Application Data Sheet

\_\_\_\_\_**AF/D**\_\_\_\_\_  
Affidavit or Exhibit Received

\_\_\_\_\_**APPENDIX**\_\_\_\_\_  
Appendix

\_\_\_\_\_**ARTIFACT**\_\_\_\_\_  
Artifact

\_\_\_\_\_**BIB**\_\_\_\_\_  
Bib Data Sheet

\_\_\_\_\_**CLM**\_\_\_\_\_  
Claim

\_\_\_\_\_**COMPUTER**\_\_\_\_\_  
Computer Program Listing

\_\_\_\_\_**CRFL**\_\_\_\_\_  
All CRF Papers for Backfile

\_\_\_\_\_**DIST**\_\_\_\_\_  
Terminal Disclaimer Filed

\_\_\_\_\_**DRW**\_\_\_\_\_  
Drawings

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Foreign Reference

\_\_\_\_\_**FRPR**\_\_\_\_\_  
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Non-Patent Literature

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\_\_\_\_\_**NOA**\_\_\_\_\_  
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\_\_\_\_\_**PETDEC**\_\_\_\_\_  
Petition Decision

## OUTGOING

\_\_\_\_\_**CTMS**\_\_\_\_\_  
Misc. Office Action

\_\_\_\_\_**1449**\_\_\_\_\_  
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\_\_\_\_\_**892**\_\_\_\_\_  
892

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\_\_\_\_\_**APDEC**\_\_\_\_\_  
Board of Appeals Decision

\_\_\_\_\_**APEA**\_\_\_\_\_  
Examiner Answer

\_\_\_\_\_**CTAV**\_\_\_\_\_  
Count Advisory Action

\_\_\_\_\_**CTEQ**\_\_\_\_\_  
Count Ex parte Quayle

\_\_\_\_\_**CTFR**\_\_\_\_\_  
Count Final Rejection

## INCOMING

\_\_\_\_\_**AP.B**\_\_\_\_\_  
Appeal Brief

\_\_\_\_\_**C.AD**\_\_\_\_\_  
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## Internal

\_\_\_\_\_**SRNT**\_\_\_\_\_  
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\_\_\_\_\_**WFEE**\_\_\_\_\_  
Fee Worksheet

## File Wrapper

\_\_\_\_\_**FWCLM**\_\_\_\_\_  
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\_\_\_\_\_**SRFW**\_\_\_\_\_  
File Wrapper Search Info

BACKFILE DOCUMENT INDEX SHEET



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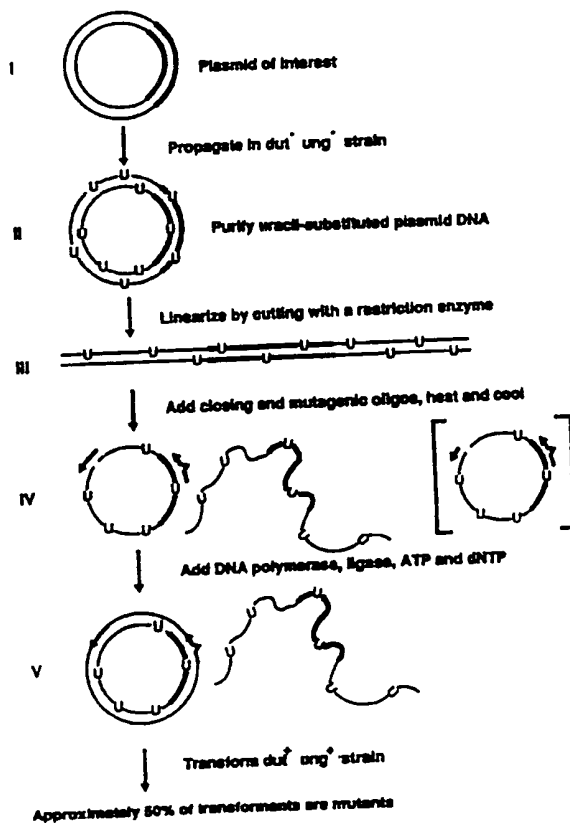
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(54) Title: PROCESS FOR CONDUCTING SITE-DIRECTED MUTAGENESIS

(57) Abstract

The present invention relates to an approach to site-directed mutagenesis of double-stranded DNA. This approach involves the generation of structures capable of directing full-length complementary-strand synthesis of DNA. The structures are formed following heat denaturation and cooling of linear DNA templates in the presence of what is a "closing" oligonucleotide. This closing oligonucleotide is a nucleotide sequence having at least part of its sequence complementary to at least one of the free ends of the DNA template. The closing oligonucleotide functions as an agent for circularization of a DNA strand and generation of a primer-circular template structure suitable for polymerase-dependent full-length complementary-strand synthesis and ligation into a covalently-closed heteroduplex DNA molecule.



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TITLE OF THE INVENTION

Process for conducting site-directed mutagenesis.

FIELD OF THE INVENTION

5 The invention relates to a process for conducting site-directed mutagenesis directly on double-stranded DNA using closing oligonucleotides capable of directing full-length complementary-strand synthesis for linearized double-stranded DNA.

BACKGROUND OF THE INVENTION

10 Because of its broad applicability, oligonucleotide-directed site-specific mutagenesis embodies a tool fundamental to modern molecular biology research. Its utilization for the introduction of insertions, deletions, and substitutions into coding or  
15 non-coding DNA permits the execution of a wide variety of investigations including analysis of structure-function relationships at the level of DNA, RNA, and protein. In the area of enzyme catalysis for example, structural and mechanistic information derived from  
20 amino acid substitutions by site-directed mutagenesis continues to add significantly to a wealth of knowledge obtained from biochemical and biophysical studies.

Following the initial reports demonstrating the use of synthetic oligonucleotides to create  
25 phenotypically selectable site-specific mutations within  $\phi$ X174 DNA, general methods for site-directed mutagenesis were put forth. Since these developments around ten years ago, many different approaches designed to reduce the time and effort necessary to construct a desired  
30 site-specific mutation have been described. In general, these methods fall into two categories: those designed to eliminate the laborious differential hybridization manipulations necessary for identification of the mutant molecules against a large background of parental forms, and the others, aimed at circumventing the requirement  
35 for cloning of the target DNA into specialized vectors for the production of single-stranded DNA templates.

An approach which maintains general applicability and high efficiency, and allows site-directed mutagenesis to be performed directly on any existing plasmid would therefore be desirable.

5     SUMMARY OF THE INVENTION

10     The present invention provides a novel approach for conducting site-directed mutagenesis directly on double-stranded DNA previously cleaved and denatured to single-stranded linear DNA templates using a closing oligonucleotide.

15     The process first comprises hybridizing mutagenic and closing oligonucleotides to single-stranded linear DNA templates. The closing oligonucleotide is characterized by having at least part of its nucleotide sequence complementary to at least one of the free ends of said linear DNA templates to direct full-length complementary-strand synthesis and circularization of the linear DNA templates.

20     Once the hybridizations have been completed, the mutagenic and closing oligonucleotides are incorporated into DNA strands complementary to the linear DNA templates and ultimately into covalently closed DNA circles by submitting the hybridized linear DNA templates to the action of polymerase and ligase enzymes to yield heteroduplex double-stranded DNA molecules.

25     Finally, the process of the present invention comprises a further step through which selective replication of the synthesized complementary strand of the heteroduplex DNA is performed. It is preferred to use uracil-substituted DNA templates obtained through propagation of the target DNA sequence in a *dut<sup>-</sup> ung<sup>-</sup>* strain of *E. coli* as a suitable selection system.

30     Optionally, the process of the present invention may itself comprise an initial step through which double-stranded DNA is cleaved and denatured to linear single-stranded DNA templates.

Preferably, the closing oligonucleotide referred to above will have at least two different portions of its nucleotide sequence complementary to each free end of the linear DNA template in order to anneal to both free ends thereof, thereby causing circularization of the DNA template. Alternatively, the closing oligonucleotide may have a sequence complementary only to the 3' end of the DNA template.

The process of the present invention may be extended to other types of investigations in which a genetically altered complementary-strand to a prokaryotic or eucaryotic autonomous plasmid or replicon is required.

Also within the scope of the present invention is a kit for conducting site-directed mutagenesis of double-stranded DNA previously cleaved and denatured to single-stranded linear DNA templates. The templates are hybridized to mutagenic and closing oligonucleotides which are in turn incorporated into DNA strands complementary to the template. The kit comprises one or more closing oligonucleotides having at least part of their nucleotide sequence complementary to at least one of the free ends of the single-stranded linear DNA templates, and means for selective replication of the complementary DNA strand. Preferably a *dut<sup>-</sup> ung<sup>-</sup>* strain of *E. coli* such as that referred to above, will be used as a selection means. The kit of the present invention may also contain the appropriate control DNA's and optionally, suitable reagents and buffers.

Finally, the present invention relates to a closing oligonucleotide to anneal to the free ends of a single-stranded linear DNA template whereby circularization of the single-stranded linear DNA template is obtained, the closing oligonucleotide being characterized by having between 10 and 50 nucleotides in length and by having a nucleotide sequence at least

complementary to the free ends of the linear DNA template.

Preferably, the closing oligonucleotide is selected from the group consisting of the following:

- 5 (AatII) 5'TGGTTTCTTAGACGTCAGGTGGCACTTTTC;  
(AflIII) 5'CTGGCCTTTTGCTCACATGTTCTTTCCTGC;  
(AseI) 5'CTTCCCGGCAACAATTAATAGACTGGATGG;  
(MstI) 5'TGGCAACAACGTTGCGCAAACCTATTAAGT;  
(NdeI) 5'GTATTTTACACCGCATATGGTGCCTCTCA;  
10 (PstI) 5'ACCACGATGCCTGCAGCAATGGCAACAACG;  
(PvuI) 5'ACTTCTGACAACGATCGGAGGACCGAAGGA;  
(ScaI) 5'ATGACTTGGTTGAGTACTCACCAGTCACAG;  
(SspI) 5'AAATGCTTCAATAATATTGAAAAAGGAAGA;  
(XmnI) 5'TCGCCCCGAAGAACGTTTCCCAATGATGAG;  
15 5'CTGTGACTGGTGAGTACTCAACCAAGTCAT;

and complementary sequences thereof.

The present invention will be more readily illustrated by referring to the following description.

#### IN THE DRAWINGS

20 Figure 1 is a schematic representation of a preferred embodiment of the sequence of steps and expected structures obtained when performing the site-directed mutagenesis reaction of the present invention.

25 Figure 2 represents the effects of increasing oligonucleotide concentrations on the efficiency of the standard complementary-strand synthesis/site-directed mutagenesis reaction of the present invention.

#### DETAILED DESCRIPTION OF THE INVENTION

30 The present invention relates to a novel approach to site-directed mutagenesis of double-stranded DNA. This approach involves the generation of structures capable of directing full-length complementary-strand synthesis of DNA. The structures are formed following heat denaturation and cooling of  
35 linear DNA templates in the presence of what will be referred to in the disclosure as a "closing" oligonucleotide. This closing oligonucleotide is a



nucleotide sequence having at least part of its sequence complementary to at least one of the free ends of the DNA template. The closing oligonucleotide functions as an agent for circularization of a DNA strand and generation of a primer-circular template structure suitable for polymerase-dependent full-length complementary-strand synthesis and ligation into a covalently-closed heteroduplex DNA molecule.

To develop this new process, it was hypothesized that the time-dependent concentration of single-stranded DNA, available following denaturation of a homogeneous population of linear double-stranded molecules, may be sufficient for use as templates in polymerase-dependent DNA synthesis reactions. Further, it was considered that, during the course of DNA synthesis, the helicase activity of polymerases (*E. coli* polymerase I, for example) may prove useful for augmenting the level of complementary-strand synthesis by effecting strand displacement in partially reannealed molecules.

Application of the foregoing conditions to actual site-directed mutagenesis experiments requires two additional elements: (i) a closing oligonucleotide, other than the mutagenic one, for directing full-length complementary-strand synthesis and circularization of the linear DNA templates, and (ii) a mechanism for selective replication of the newly synthesized strand in order to obtain high efficiency of mutagenesis.

#### Closing oligonucleotides

The use of what has been termed a "closing" oligonucleotide meets the requirements for a primer invariably necessary for handling the problem of making full-length copies of linear DNA templates and providing for the resultant double-stranded molecules to be converted into covalently-closed circles by the action of DNA ligase.

Conceptually, two forms of a closing oligonucleotide are possible: an "overlapping" form, which spans the site of linearization by annealing to the free ends of the template strand thereby causing circularization of the DNA strand; or alternatively, a "flush" form which would produce blunt-ended molecules by hybridizing directly to the 3' end of the target template strand. In both cases, the closing oligonucleotide may contain between 10 and 50 nucleotides.

The dependence of this new approach on the use of a closing oligonucleotide and the availability of a unique restriction enzyme site can be met in a general way by designing the closing oligonucleotide to hybridize at any restriction enzyme site with a sequence common to most DNA sequences, such as the plasmid pBR322-derived  $\beta$ -lactamase gene and *colE1* replication origin. For example, a closing oligonucleotide may be constructed to span the *Pst*I, *Pvu*I or *Sca*I sites in the  $\beta$ -lactamase gene or the *Afl*III or *Nde*I site near the origin of replication. In the event any of these sites occur more than once in a particular DNA sequence of interest, linearization may be performed by partial digestion without risk of adversely affecting the reaction since uncleaved, incorrectly cleaved and extensively cleaved molecules have little or no transformation capacity under the present conditions.

The type of oligonucleotide design referred to above would therefore enable the preparation of a single closing oligonucleotide to be employed as a common reagent for a large variety of mutagenesis experiments.

#### Selection system

For a selection system, the use of parental DNA which has been uracil-substituted provides a simple and convenient biological approach for preferential survival of the newly synthesized complementary DNA strand and therefore high efficiency mutagenesis.

Uracil-substituted DNA is prepared by propagating the desired DNA template in an *E.coli* *dut*<sup>-</sup> *ung*<sup>-</sup> strain. *dut*<sup>-</sup> *ung*<sup>-</sup> strains are deficient in the enzyme dUTPase, the product of the *dut* gene, resulting in an increased intracellular pool of dUTP which competes with TTP for incorporation into DNA. Also, uracil incorporated into the DNA strand is not removed because of the deficiency of the *dut*<sup>-</sup> *ung*<sup>-</sup> strain in producing uracil glycosylase, the enzyme responsible for cleavage of the uracil nucleotides and coded for by the *ung* gene.

Thus, uracil-substituted DNA is biologically active in a *ung*<sup>-</sup> strain incapable of removing uracil. However, the biological activity of uracil-substituted DNA templates is substantially decreased when this DNA is introduced in a *ung*<sup>+</sup> host, which will deactivate the template through the action of uracil glycosylase.

As previously shown by Kunkel in *Proc. Natl. Acad. Sci. USA* 82, 488-492 (1985), propagation of a single-stranded target DNA in a *dut*<sup>-</sup> *ung*<sup>-</sup> strain of *E. coli* yields uracil-containing templates whose efficiency in transforming *dut*<sup>+</sup> *ung*<sup>+</sup> strains is 3 to 4 orders of magnitude lower than that of normal DNA. However, in vitro synthesis of a mutagenic strand complementary to the uracil-substituted template through a mutagenic oligonucleotide will lead to a complementary strand free of uracil. This uracil-free complementary strand is still biologically active in a *dut*<sup>+</sup> *ung*<sup>+</sup> strain of *E.coli*, even after having been treated with uracil glycosylase prior to transfection, whereas the uracil-containing templates will have been deactivated by such a treatment. Using this method in the context of the present invention, a significant level of transformation efficiency is obtained and 40 to 60% of the transformants have the mutant phenotype.

In fact, the combined use of a closing oligonucleotide to hybridize to a single-stranded DNA template generated from linearized and denatured DNA,

and the *dut<sup>-</sup> ung<sup>-</sup>* strain of *E. coli*, provides a process which allows site-directed mutagenesis to be performed directly on double-stranded DNA with a mutant formation efficiency of approximately 50%, a level amenable to rapid screening by DNA sequencing.

However, those skilled in the art will readily appreciate that other selection systems such as incorporation of thionucleotides described by Taylor et al., in *Nucl. Acids Res.* 13, 8749-8785, (1985) or differential methylation may potentially be used in the context of the present invention.

Site-directed mutagenesis using the process of the present invention with a *dut<sup>-</sup> ung<sup>-</sup>* strain of *E. coli* as a selection system

In order to perform the desired mutagenic reaction on a target DNA strand, the strand in question is first propagated in a *dut<sup>-</sup> ung<sup>-</sup>* strain of *E. coli* and isolated using any suitable technique known to those skilled in the art. Once the desired DNA sequence has been isolated and purified, it is linearized by being reacted with a suitable restriction enzyme if it is in circular form, and subsequently brought to single-stranded form by heat denaturation.

The template DNA thus obtained, will be mixed with the desired closing and mutagenic oligonucleotides. A suitable annealing buffer is added and the reaction mixture may be incubated at a temperature ranging from 70 to 100°C for a time period ranging from 0.5 to 5 minutes, then optionally cooled at a temperature ranging from 0 to 42°C for a period ranging from 1 to 15 minutes.

After cooling, a suitable DNA synthesis buffer, DNA ligase and a polymerase are added and the mixture may be incubated at a temperature ranging from 0 to 42°C for a period ranging from 1 to 5 hours.

The mixture, which contains complete mutagenic DNA strands hybridized to their complementary uracil-substituted DNA templates is then stored at a

temperature ranging from 0 to 10°C or used directly to transform the desired *dut<sup>+</sup> ung<sup>+</sup>* cells. The preparation of competent cells and transformation reactions will be performed according to procedures well known in the art, although the method of Hanahan described in *J. Mol. Biol.* 166, 557-580 (1983) is preferred. Following the transformation, the cells harboring the mutagenic DNA strands are selected.

The present invention will be more readily illustrated by referring to the following example.

#### Example 1

Mutagenesis on color indicator systems based on the  $\alpha$ -complementation of  $\beta$ -galactosidase.

In order to test the approach of the present invention and to quantitatively evaluate its potential for complementary-strand synthesis and concomitant site-directed mutagenesis, two color indicator systems based on the  $\alpha$ -complementation activity of  $\beta$ -galactosidase (*lacZ $\alpha$* ) were developed.

The system referred to as B2W (blue-to-white) employs a mutagenic oligonucleotide to convert the blue chromogenic plasmid pUC19 described in *Gene* 33, 103-119 (1985) into a colorless plasmid by altering 2 bases to generate a TAA termination codon 29 amino acids downstream from the start of *lacZ $\alpha$*  translation. Simultaneously, a *Dra*I site is created for verification of the presence of the intended changes.

In the second system, referred to as W2B (white-to-blue), the mutagenic oligonucleotide inserts 2 bases into plasmid pSNS282, a colorless derivative of plasmid pUC19. Plasmid pSNS282 was constructed by cleavage of pUC19 DNA with *Hind*III followed by treatment with Klenow polymerase to fill in the staggered ends and T4 DNA ligase to recircularize the molecules. Following transformation into JM110 as described in *Gene* 33, 103-119 (1985), colorless colonies on plates containing 30

5 uM isopropyl thiogalactoside (IPTG) and 30 µg/ml 5-bromo-4-chloro-3-indolyl-β-D-galactoside (X-Gal) were analyzed for the presence of a newly created *NheI* recognition sequence, a subset of which is the in-frame  
10 amber triplet (...A AGC TAG CTT...). The 2-base insertion into pSNS282 created by the mutagenic oligonucleotide eliminates the amber codon and leads to a reading frame yielding production of blue colonies. Simultaneous generation of a restriction enzyme site, *XhoI*, was also included in the system design.

#### Generation of linear DNA templates

Both plasmids were first propagated in the dut<sup>-</sup> ung<sup>-</sup> RZ1032 strain (ATCC # 39737) described by Kunkel in *Proc. Natl. Acad. Sci., USA* 82, 488-492 (1985), to yield  
15 uracil-substituted plasmid DNA. The cultures harbouring either pUC19 or pSNS282 were grown overnight in a medium containing 1.6% Bactotryptone, 1% Yeast Extract, 0.5% NaCl and 100 µg/ml ampicillin. The resulting uracil-substituted plasmids were then purified by equilibrium  
20 centrifugation in CsCl-ethidium bromide step-gradients as described in *Biochem. Biophys. Res. Commun.* 117, 835-842 (1983). Linearized uracil-substituted templates were prepared by cleavage of the DNA with *ScaI* followed by extraction with phenol, precipitation with ethanol  
25 and resuspension at 50 ng/µl in 1 mM Tris-HCl, pH 8.0, and 0.1 mM EDTA.

#### Preparation of the closing and mutagenic oligonucleotides

The two closing oligonucleotides,  
30 5'-CTGTGACTGGT-GAGTACTCAACCAAGTCAT (overlapping) and 5'-ACTCAACCAAGTCATT-CTGAG (flush); and the two mutagenic oligonucleotides, 5'-CCCAGTCACGACGTTTTT**AA**CGACGGCCAGTG (B2W, mismatched bases underlined, *DraI* site in bold) and 5'-GCAGGCATGCAAGCT**CGAG**-CTTGGCGTAATCA (W2B, insertion  
35 bases underlined, *XhoI*, site in bold) were synthesized by the phosphoramidite method using an Applied Biosystems Model 380B DNA synthesizer. Purification of

oligonucleotides was performed by precipitation from 2.5 M ammonium acetate-83% ethanol followed by washing with 95% ethanol at room temperature. Purified oligonucleotides were phosphorylated as described in Maniatis et al., *Molecular Cloning, Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York. Both the B2W and W2B systems utilize the same closing oligonucleotides which were designed for interaction at the unique *ScaI* site in the  $\beta$ -lactamase gene.

Although the above-mentioned closing and mutagenic oligonucleotides represent the embodiments used in this example, those skilled in the art will readily appreciate that the present invention is not limited to the use of these oligonucleotides sequences and complementary sequences thereof. The following closing oligonucleotides and complementary sequences thereof also fall within the scope of the present invention:

20	(AatII)	5'TGGTTTCTTAGACGTCAGGTGGCACTTTTC;
	(AflIII)	5'CTGGCCTTTTGCTCACATGTTCTTTCCTGC;
	(AseI)	5'CTTCCCGGCAACAATTAATAGACTGGATGG;
	(MstI)	5'TGGCAACAACGTTGCGCAAACCTATTAAC TG;
	(NdeI)	5'GTATTTACACCCGCATATGGTGCACCTCTCA;
25	(PstI)	5'ACCACGATGCCTGCAGCAATGGCAACAACG;
	(PvuI)	5'ACTTCTGACAACGATCGGAGGACCGAAGGA;
	(ScaI)	5'ATGACTTGGTTGAGTACTCACCAGTCACAG;
	(SspI)	5'AAATGCTTCAATAATATTGAAAAAGGAAGA;
	(XmnI)	5'TCGCCCCGAAGAACGTTTTCCAATGATGAG;

30 However, it is to be understood that these typical examples of closing oligonucleotides are introduced to illustrate rather than limit the scope of the present invention. In fact, any oligonucleotide having the ability to hybridize to at least the free ends of either a linear DNA strand or a circular DNA strand previously digested at a common restriction site can be used in the context of the present invention.

35

Standard complementary-strand synthesis/site-directed mutagenesis protocol.

Unless indicated otherwise, reactions were performed as follows. 0.1 pmole of template DNA was mixed with 2 pmoles of closing oligonucleotide and 10 pmoles of mutagenic oligonucleotide and the final volume adjusted to 22  $\mu$ l with water. To this mixture, 3  $\mu$ l of annealing buffer (200 mM Tris-HCl, pH 7.4, 20 mM MgCl<sub>2</sub>, and 500 mM NaCl) was added and the mixture was incubated in a boiling water bath for 3 minutes then transferred to ice. After incubation on ice for 2 to 8 minutes, 3  $\mu$ l of DNA synthesis buffer (300 mM Tris-HCl, pH 7.8, 80 mM MgCl<sub>2</sub>, 100 mM DTT, 10 mM ATP, 5 mM each of dGTP, dATP, dTTP and dCTP, and 500  $\mu$ g/ml BSA), 1  $\mu$ l of T4 DNA ligase (1 u/ $\mu$ ), and 1  $\mu$ l of Klenow polymerase (7 u/ $\mu$ l) were added and incubation on ice continued for an additional 30 minute period. The reaction mixture was then transferred sequentially to room temperature for 30 minutes and 37°C for 60 minutes. At this point, the reaction mixture was either stored at 4°C or one half of their final volume used directly to transform 200  $\mu$ l of competent HB2151 *E. coli* cells. Preparation of competent cells and transformation reactions were performed according to the method of Hanahan referred to above. The density of the various competent cells batches was pre-adjusted such that 200  $\mu$ l of competent cells gave an efficiency of about  $1 \times 10^6$  transformants per  $\mu$ g of pUC19 DNA. One tenth of the final transformation volume (100  $\mu$ l) was spread onto rich plates containing 100  $\mu$ g/ml ampicillin, 30  $\mu$ M IPTG and 30  $\mu$ g/ml X-Gal. The number of blue and white colonies was counted and the relative proportion of mutants expressed as a percentage of the total.

A schematic representation of the sequence of steps and expected structures for the standard site-directed mutagenesis reaction is shown in Figure 1 where the target gene for mutagenesis is indicated by a heavy



line. Uracil-substituted DNA strands are represented by a line with an occasional "u". The oligonucleotides are also shown as a heavy line with an arrowhead at the 3' end. The mutagenic oligonucleotide contains an inflection denoting the mismatch. In brackets, the expected structure for the "flush" closing oligonucleotide is depicted; that for the more effective "overlapping" closing oligonucleotide is shown in the main body of the figure (structure IV).

10 Characterization of the complementary-strand synthesis and site-directed mutagenesis process of the present invention

15 Characterization of the process of the present invention was initially performed by evaluating the transformation efficiency of the standard uracil-substituted, linear templates (Figure 1, structure III) with or without treatment with various complementary-strand synthesis components.

20 Reactions were carried out as described above including all buffers and manipulations but containing only the indicated DNA synthesis components. The concentrations per reaction were 0.1 pmole of standard template (linearized, uracil-substituted pUC19 or pSNS282 DNA), 2 pmole of oligonucleotide, and 7 units of the Klenow enzyme and 1 unit of T4 DNA ligase, as required.

25 Results are summarized in Table 1 below, where the values given are an average of 7 experiments.

30

35

TABLE 1

Complementary-strand formation as indicated  
by DNA synthesis-dependent increase in the  
transformation efficiency of  
linearized uracil-substituted DNA

Reaction components	Colonies per plate
Template	3
Template + overlapping closing oligo	5
Template + flush closing oligo	0
Template + polymerase and ligase	4
Template + overlapping closing oligo + polymerase and ligase	88
Template + flush closing oligo + polymerase and ligase	23

5 It can be seen from this table that only conditions which support DNA synthesis result in enhanced efficiency of transformation. In the absence of DNA synthesis, the number of transformants observed is close to zero, indicating that the template itself, even in combination with other components of the reaction, contributes minimally to the background.

10 Table 1 also shows that the overlapping closing oligonucleotide is nearly 4-fold more effective than the flush closing oligonucleotide (Figure 1, structure IV) in producing transformation competent molecules. The reason for this may be related to enhanced ligation efficiency and better protection of the free ends of the template strand by the overlapping structure. Because of its greater effectiveness, the

15

overlapping closing oligonucleotide was selected for use in all subsequent experiments.

Further evidence for full-length complementary-strand synthesis and the evaluation of the present strategy for application to site-directed mutagenesis were obtained by performing complete reactions (Figure 1) using the B2W and W2B test systems. The experiments were performed as described above using 0.1 pmole template, 2 pmole overlapping closing oligonucleotide and 10 pmole mutagenic oligonucleotide. Results are shown in Table 2 where the values given are an average of 16 and 9 independent experiments for the B2W and W2B systems, respectively.

TABLE 2

Site-directed mutagenesis of the two test systems, B2W and W2B, by complementary-strand synthesis using double-stranded DNA templates.

System	Colonies per plate	% Mutants
B2W	62	49
W2B	57	31

The data in Table 2 show that inclusion of a mutagenic oligonucleotide appropriately alters the phenotype of the newly synthesized strand at high frequencies. The lower mutant formation efficiency observed for the 2-base insertion mutagenesis in the W2B system is presumably a consequence of a weaker mutagenic oligonucleotide-template duplex since such lower efficiency could be improved by elevation of

oligonucleotide concentration as shown in Figure 2, where Panel A shows the number of colonies obtained as a function of increasing concentrations of the overlapping closing oligonucleotide. Standard reactions were carried out as described above using 0.1 pmoles of linearized pUC19 or pSNS282 uracil-substituted DNA templates and no mutagenic oligonucleotides. Panel B shows the effects of increasing concentrations of the B2W (triangles) or W2B (circles) mutagenic oligonucleotides on the efficiency of site-directed mutagenesis. Reactions using components of the B2W or W2B system were performed as described above using 0.1 pmoles of template DNA and 2 pmoles of overlapping closing oligonucleotide.

In order to verify the presence of the intended alterations, plasmid DNA from mutant colonies selected at random and from different site-directed mutagenesis reactions using the B2W and W2B systems, were cleaved by the restriction enzymes *DraI* and *XhoI*, respectively. All mutant colonies tested yielded plasmid DNA containing the appropriate concomitantly created restriction enzyme site. Moreover, no plasmid rearrangement or multiple introduction of the restriction sites had taken place as indicated by these and other restriction enzyme analyses. Characteristics and requirements of the site-directed mutagenesis reaction.

Table 3 shows the results of experiments in which the dependence of site-directed mutagenesis on the individual components or treatment steps of the standard reaction protocol was explored.

Reactions were carried out as described above except that the indicated component or step was omitted. The values given are an average of 3 independent experiments.

TABLE 3

Characteristics and requirements of the site-directed mutagenesis reaction.

Component/Step	B2W system		W2B system	
	Colonies	% Mutants	Colonies	% Mutants
Complete reaction	64	46	47	30
No template	0	--	0	--
No closing oligo	5	--	4	--
No mutagenic oligo	51	--	47	--
No annealing buffer	0	--	0	--
No polymerase	4	--	17	--
No ligase	0	--	2	--
No denaturation step	7	--	1	--
No ice incubation step <sup>a</sup>	44	56	53	37
No RT incubation step <sup>b</sup>	30	40	14	15
No 37°C incubation step <sup>c</sup>	53	53	40	35

a Following the denaturation step, the reaction was placed at room temperature; and after the addition of dNTP, polymerase and ligase, it was kept at room temperature for 60 min. then transferred to 37°C for 60 min.

b At the end of the 30 min. incubation period on ice, this reaction was transferred directly to 37°C.

c For this reaction, the last 60 min. at 37°C was replaced by 60 min. at room temperature.

It is evident that omission of any one of the reaction components or the template denaturation step results in complete loss of mutant formation activity. On the other hand, elimination of the ice and/or 37°C incubation steps appears to slightly improve the frequency of mutant molecules.

The activity of several DNA polymerases other than the Klenow enzyme has also been evaluated under standard conditions. As judged by the number of transformants and the relative proportion of mutant colonies obtained, *E. coli* polymerase I functioned about as well as the Klenow fragment, while T4 and T7 polymerase were less effective. M-MLV reverse transcriptase and Taq polymerase gave little or no activity under the experimental conditions set forth above. However, it is to be understood by those skilled in the art that variations of one or more of the experimental parameters could lead to substantial increases in those instances where enzymatic activity is weak or non-existent.

The potential of covalently-closed circular DNA for use as substrates under the present site-directed mutagenesis conditions has also been examined. In order to do so, uracil-containing supercoiled DNA was substituted for the linear template DNA and subjected to site-directed mutagenesis (B2W system without a closing oligonucleotide) using the standard reaction conditions or the standard conditions in which alkaline instead of heat denaturation was performed. The results of several independent experiments revealed that only 5 to 10% of the transformants have the mutant phenotype. The reason for this reduced frequency of mutagenesis is due to a substantial increase in the level of the background and perhaps to a larger extent on inefficient and/or incomplete complementary-strand synthesis. It may be possible to improve the efficiency of mutagenesis using uracil-substituted supercoiled templates and the present

5 conditions for complementary-strand synthesis by  
treatment of the heteroduplex with uracil glycosylase  
and alkali to reduce the background as shown in *Proc.*  
*Natl. Acad. Sci., USA* 82, 488-492 (9185) or by  
introducing a single-stranded nick in the DNA as  
described in *Science* 209, 1396-1400 (9180), in order to  
generate usable circular templates.

10 The process of the present invention has been  
successfully applied to plasmid systems other than the  
B2W and W2B test systems and appears to be of general  
applicability as shown in Table 4.

TABLE 4  
Mutations introduced.

Plasmid	Size, kilobases	Gene mutated	Mutation introduced	Length of oligo	Screening method	Efficiency of mutagenesis
pUC19	2.8	<i>lacZα</i>	TAC-- AAA	33	color/RE	50 (see text)
PSNS282	2.8	<i>lacZα</i>	TA-- TCGA	32	color/RE	30 (see text)
pJWL184	4.0	LexA	AT-- CC	32	RE	44 (4/9)
pJWL184	4.0	LexA	AG-- CC	32	RE	33 (4/12)
pGEM-TAC-ONCO	3.5	Oncomodulin	A-- T	22	Sequencing	66 (4/6)
pGEM-TAC-ONCO	3.5	Oncomodulin	AA-- TG	21	Sequencing	60 (3/5)

The mutagenesis reactions were performed as described above using the overlapping closing oligonucleotide.

The plasmids pUC19, pJWL184 and pGEM-TAC-ONCO respectively described in Yanisch-Perron, C., Vieira, J., and Messing, J. (1985) Gene 33, 103-119, Lin, L-L., and Little, J.W. (1988) J. Bacteriol. 170, 2163-2173 and MacManus, J.P., Hutnik, C.M.L., Sykes, B.D. Szabo, A.G., Williams, T.C., and Banville, D. (1989) J. Biol. Chem. 264, 3470-3477, have been constructed in other works; PSNS282 was constructed as described above.

RE indicates that screening was performed by checking for a newly created restriction enzyme site.

The values given are the percentage of mutants followed in parentheses by the number of mutants obtained out of the total screened.



CLAIMS

1. A process for conducting site-directed mutagenesis on double-stranded DNA previously cleaved and denatured to single-stranded linear DNA templates, said process comprising
- 5 (a) hybridizing mutagenic and closing oligonucleotides to single-stranded linear DNA templates, said closing oligonucleotide being characterized by having at least part of its nucleotide sequence complementary to at least one of the free ends of said linear DNA templates,
- 10 (b) incorporating said mutagenic and closing oligonucleotides into DNA strands complementary to said linear DNA templates by submitting said hybridized linear DNA templates to the action of polymerase and ligase enzymes to yield heteroduplex double-stranded DNA molecules, and
- 15 (c) selectively replicating said complementary DNA strands of said heteroduplex double-stranded DNA.
- 20 2. A process according to claim 1, which further comprises an initial step through which said double-stranded DNA is cleaved and denatured to yield single-stranded linear DNA templates.
- 25 3. A process according to claim 1, wherein said double-stranded DNA is a plasmid or any autonomous replicon.
4. A process according to claim 1, wherein said closing oligonucleotide has a nucleotide sequence at least complementary to the free ends of said linear DNA templates to anneal to both free ends of said linear DNA templates upon hybridization to cause circularization of said linear DNA templates.
- 30 5. A process according to claim 1, wherein said closing oligonucleotide has a sequence complementary to the 3' end of said linear DNA templates
- 35

thereby creating blunt-ended molecules upon hybridization to said linear DNA templates.

6. A process according to claim 1, wherein said complementary DNA strands are selectively replicated by initially propagating said double-stranded DNA in a *dut<sup>-</sup> ung<sup>-</sup>* bacterial strain to obtain uracil-substituted DNA templates and then transforming said heteroduplex DNA molecules into a *dut<sup>+</sup> ung<sup>+</sup>* bacterial strain to obtain the desired mutant molecules.

7. A process according to claim 1, wherein said closing oligonucleotides are selected from the group consisting of the following:

(AatII) 5'TGGTTTCTTAGACGTCAGGTGGCACTTTTC;  
(AflIII) 5'CTGGCCTTTTGCTCACATGTTCTTTCCTGC;  
(AseI) 5'CTCCCGGCAACAATTAATAGACTGGATGG;  
(MstI) 5'TGGCAACAACGTTGCGCAAACCTATTAACG;  
(NdeI) 5'GTATTTTCACACCGCATATGGTGCACTCTCA;  
(PstI) 5'ACCACGATGCCTGCAGCAATGGCAACAACG;  
(PvuI) 5'ACTTCTGACAACGATCGGAGGACCGAAGGA;  
(ScaI) 5'ATGACTTGTTGAGTACTCACCAGTCACAG;  
(SspI) 5'AAATGCTTCAATAATATTGAAAAGGAAGA;  
(XmnI) 5'TCGCCCCGAAGAACGTTTCCAATGATGAG;  
5'CTGTGACTGGTGAGTACTCAACCAAGTCAT;

and complementary sequences thereof.

8. A kit for conducting site-directed mutagenesis of double-stranded DNA previously cleaved and denatured to single-stranded linear DNA templates, said templates being hybridized to mutagenic and closing oligonucleotides incorporated into DNA strands complementary to said templates, said kit comprising:

(a) one or more closing oligonucleotides having at least part of their nucleotide sequence complementary to at least one of the free ends of said linear DNA templates, and

(b) means for selective replication of said complementary DNA strands.

9. A kit according to claim 8, wherein said closing oligonucleotides are selected from the group consisting of the following:

5 (AatII) 5'TGGTTTCTTAGACGTCAGGTGGCACTTTTC;  
(AflIII) 5'CTGGCCTTTTGCTCACATGTTCTTTCCTGC;  
(AseI) 5'CTTCCCGGCAACAATTAAGACTGGATGG;  
(MstI) 5'TGGCAACAACGTTGCGCAAACCTATTAACGT;  
(NdeI) 5'GTATTTACACCGCATATGGTGCCTCTCA;  
(PstI) 5'ACCACGATGCCTGCAGCAATGGCAACAACG;  
10 (PvuI) 5'ACTTCTGACAACGATCGGAGGACCGAAGGA;  
(ScaI) 5'ATGACTTGGTTGAGTACTCACCAGTCACAG;  
(SspI) 5'AAATGCTTCAATAATATTGAAAAGGAAGA;  
(XmnI) 5'TCGCCCCGAAGAACGTTTCCAATGATGAG;  
5'CTGTGACTGGTGAGTACTCAACCAAGTCAT;

15 and complementary sequences thereof.

10. A kit according to claim 8, wherein said closing oligonucleotides have a nucleotide sequence at least complementary to the free ends of said linear DNA templates to anneal to both free ends of said linear DNA  
20 templates upon hybridization to cause circularization of said linear DNA templates.

11. A kit according to claim 8, wherein said means for selective replication of the mutant plasmid is selected from propagation of said double-stranded DNA in  
25 a *dut<sup>-</sup> ung<sup>-</sup>* bacterial strain, incorporation of thionucleotides into said complementary DNA strands, or differential methylation

12. A closing oligonucleotide to anneal to the free ends of a single-stranded linear DNA template  
30 whereby circularization of said single-stranded linear DNA template is obtained, said closing oligonucleotide being characterized by having between 10 and 50 nucleotides in length and by having a nucleotide sequence at least complementary to the free ends of said  
35 linear DNA template.

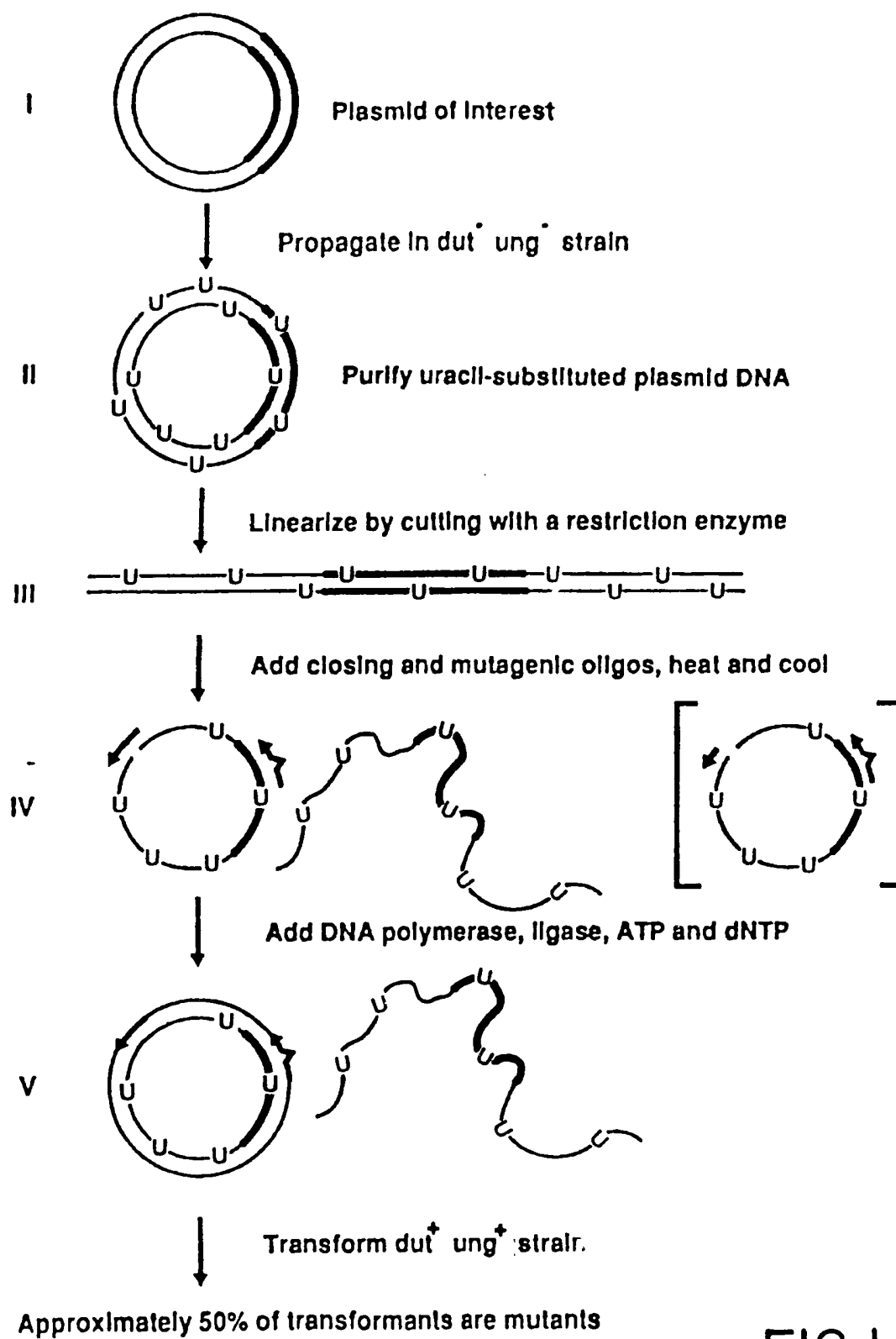


FIG. 1

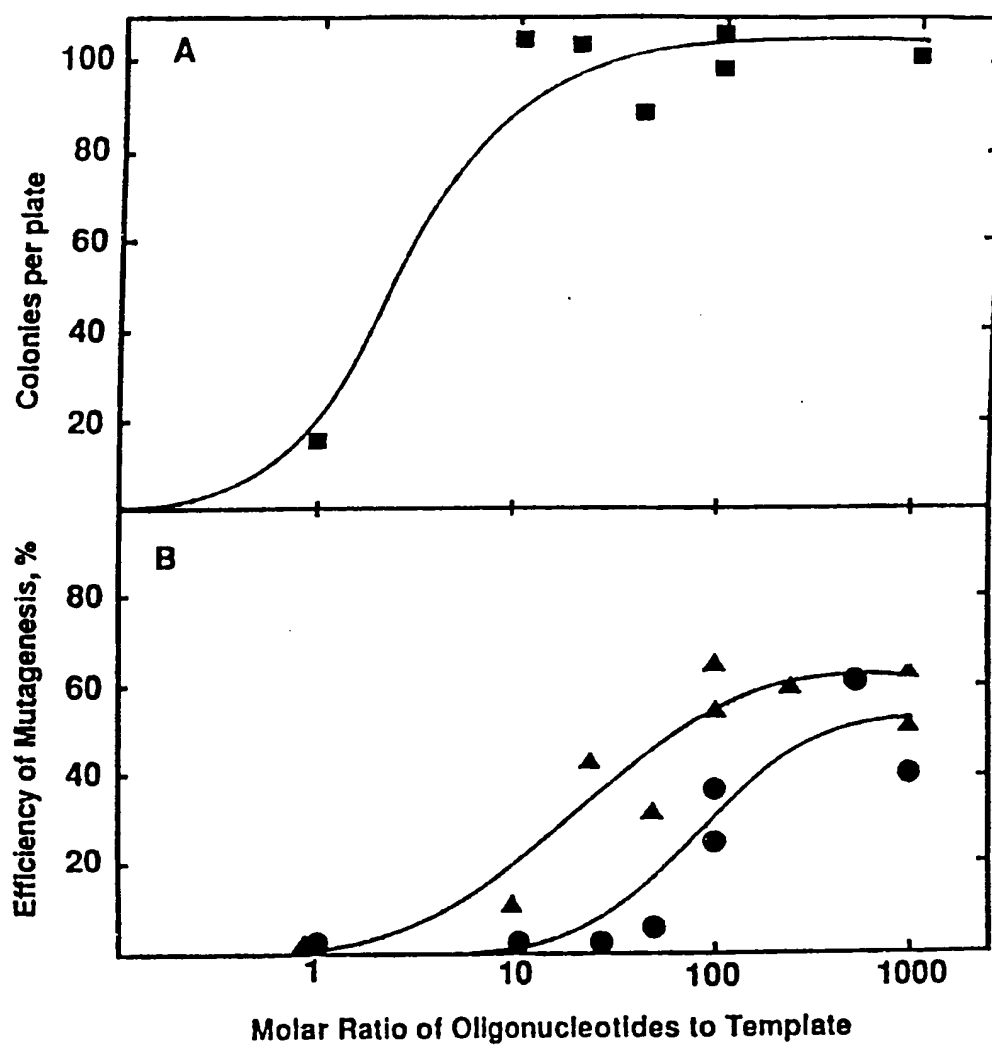
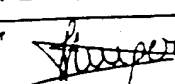


FIG. 2

# INTERNATIONAL SEARCH REPORT

SEARCH REPORT  
International Application No PCT/CA 90/00369.

<b>I. CLASSIFICATION OF SUBJECT MATTER</b> (if several classification symbols apply, indicate all) *		
According to International Patent Classification (IPC) or to both National Classification and IPC		
IPC <sup>5</sup> : C 12 N 15/10		
<b>II. FIELDS SEARCHED</b>		
		Minimum Documentation Searched <sup>7</sup>
Classification System	Classification Symbols	
IPC <sup>5</sup>	C 12 N	
Documentation Searched other than Minimum Documentation to the extent that such Documents are included in the Fields Searched <sup>8</sup>		
<b>III. DOCUMENTS CONSIDERED TO BE RELEVANT<sup>9</sup></b>		
Category <sup>*</sup>	Citation of Document, <sup>11</sup> with indication, where appropriate, of the relevant passages <sup>12</sup>	Relevant to Claim No. <sup>13</sup>
P,X	Analytical Biochemistry, vol. 185, 1990, Academic Press, Inc., S.N. Slilaty et al.: "Site-directed mutagenesis by complementary-strand synthesis using a closing oligonucleo- tide and double-stranded DNA templates", pages 194-200 see the whole article --	1-12
Y	EP, A, 0319759 (ABBOTT LABORATORIES) 14 June 1989 see summary; claim 2 --	1-12
Y	DNA, vol. 7, no. 8, 1988, Mary Ann Liebert, Inc., Publishers, M.A. Hayden et al.: "Gene synthesis by serial cloning of oligonucleotides", pages 571-577 see figure 1; discussion --  . / .	1-12
<p>* Special categories of cited documents: <sup>10</sup></p> <ul style="list-style-type: none"> <li>"A" document defining the general state of the art which is not considered to be of particular relevance</li> <li>"E" earlier document but published on or after the international filing date</li> <li>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</li> <li>"O" document referring to an oral disclosure, use, exhibition or other means</li> <li>"P" document published prior to the international filing date but later than the priority date claimed</li> <li>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</li> <li>"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</li> <li>"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</li> <li>"A" document member of the same patent family</li> </ul>		
<b>IV. CERTIFICATION</b>		
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15th January 1991	18 FEB 1991	
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III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		
Category *	Citation of Document, " with indication, where appropriate, of the relevant passages	Relevant to Claim No.
P,Y	<p>Proc. Natl. Acad. Sci. USA, vol. 82, January 1985, T.A. Kunkel: "Rapid and efficient site- specific mutagenesis without phenotypic selection", pages 488-492 see results; discussion</p> <p>-----</p>	1-12

CA 9000369  
SA 40949

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP-A- 0319759	14-06-89	JP-A- 2002348	08-01-90





A DOCPHOENIX

## APPL PARTS

           IMIS             
Internal Misc. Paper

           LET.             
Misc. Incoming Letter

           371P             
PCT Papers in a 371 Application

           A...             
Amendment Including Elections

           ABST             
Abstract

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Application Data Sheet

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Affidavit or Exhibit Received

           APPENDIX             
Appendix

           ARTIFACT             
Artifact

           BIB             
Bib Data Sheet

           CLM             
Claim

           COMPUTER             
Computer Program Listing

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Specification

           SPEC NO             
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## OUTGOING

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Misc. Office Action

           1449             
Signed 1449

           892             
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Abandonment

           APDEC             
Board of Appeals Decision

           APEA             
Examiner Answer

           CTAV             
Count Advisory Action

           CTEQ             
Count Ex parte Quayle

           CTFR             
Count Final Rejection

           CTNF             
Count Non-Final

           CTRS             
Count Restriction

           EXIN             
Examiner Interview

           M903             
DO/EO Acceptance

           M905             
DO/EO Missing Requirement

           NFDR             
Formal Drawing Required

           NOA             
Notice of Allowance

           PETDEC             
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## INCOMING

           AP.B             
Appeal Brief

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Applicant Remarks in Amendment

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## File Wrapper

           FWCLM             
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           SRFW             
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## Internal

           SRNT             
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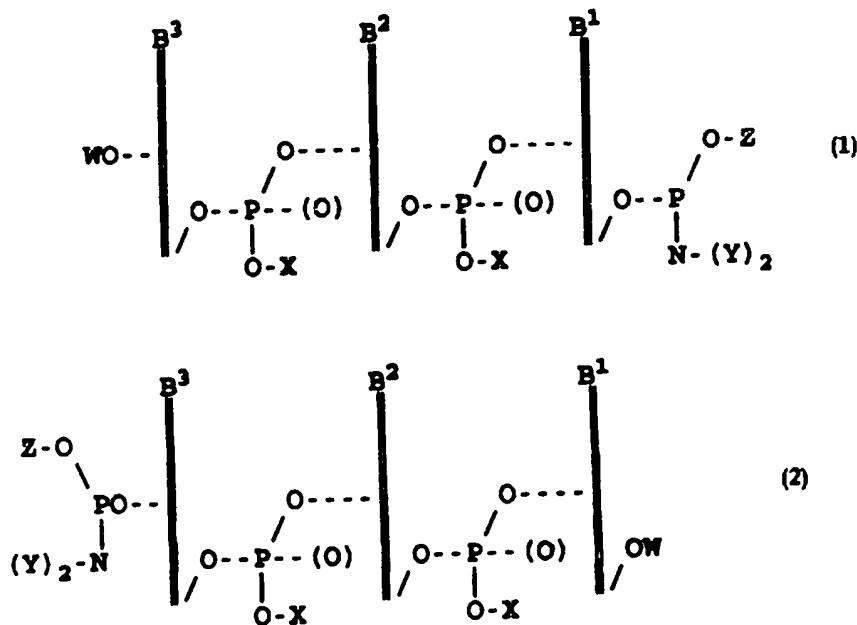
INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification<sup>6</sup> : C07H 21/00, C12N 15/11</p>	<p>A2</p>	<p>(11) International Publication Number: <b>WO 96/16073</b> (43) International Publication Date: 30 May 1996 (30.05.96)</p>
<p>(21) International Application Number: PCT/US95/15319 (22) International Filing Date: 22 November 1995 (22.11.95) (30) Priority Data: 08/344,820 23 November 1994 (23.11.94) US (71) Applicant: TERRAPIN TECHNOLOGIES, INC. [US/US]; 750-H Gateway Boulevard, South San Francisco, CA 94080 (US). (72) Inventors: LYTTLE, Matthew, H.; P.O. Box 1116, Point Reyes Station, CA 94956 (US). KAUVAR, Lawrence, M.; 1205 Cole Street, San Francisco, CA 94117 (US). (74) Agents: DROST, Patricia, M. et al.; Morrison &amp; Foerster, 2000 Pennsylvania Avenue, N.W., Washington, DC 20006 (US).</p>		<p>(81) Designated States: AU, CA, JP, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i></p>

(54) Title: CODON AMIDITES AND METHOD OF USING THEM TO PRODUCE OLIGONUCLEOTIDES AND MUTAGENESIS LIBRARIES

(57) Abstract

Compounds of formula (1) or (2) wherein W, X, Y and Z are each independently hydrogen or a protecting group; B<sup>1</sup>, B<sup>2</sup> and B<sup>3</sup> are each independently a base selected from the group consisting of adenine, guanine, cytosine, thymine and uracil; and || is the residue of a ribose or deoxyribose, and methods for their synthesis and use are disclosed.



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**CODON AMIDITES AND METHOD OF USING THEM TO  
PRODUCE OLIGONUCLEOTIDES AND MUTAGENESIS LIBRARIES**

**Technical Field**

The invention relates to the synthesis of various types of oligonucleotides that are useful in analysis, therapy and other applications. More specifically, the invention concerns a technique for using preassembled 3'-phosphoramidite trinucleotides as building blocks to make oligonucleotides encoding a desired sequence of amino acids, optionally containing positions with random amino acids. Randomized DNA fragments, in particular, are useful in producing combinatorial libraries of peptides or proteins with a variety of binding properties, from which molecules of special interest can be selected.

In one popular format, a DNA fragment is synthesized corresponding to the sequence of a bacteriophage coat protein with an appended "scrambled region" where all possible codons will be presented. This fragment family is then inserted into phage DNA such that, in an appropriate host cell population, a library of different expressed peptide regions is created. Selection of phage with desirable characteristics can then be accomplished by a variety of criteria, and the sequence responsible can be determined by sequencing the appropriate portion of the phage DNA.

**Background Art**

Use of molecular biology techniques to encode randomized sets of short peptides, of interest for their own sake or as a means to modify specific sites within protein domains, are useful to select molecules with desirable binding specificities. Trinucleotides carrying certain protecting groups have long been used as intermediates to synthesize oligonucleotides corresponding to specific peptides of interest. For example, see Wakabayashi et al., "Rapid Synthesis of Oligodeoxynucleotides by using N-Methylimidazole as a Condensation Catalyst. Syntheses of Dodecanucleotides Corresponding to Complementary Deoxyribonucleic Acid of the

- 2 -

Tetrapeptide Fragments of Cholecystokinin-Pancreozymin and Vasoactive Intestinal Peptide", Chem. Pharm. Bull., **30**, 3951-58 (1982).

Certain dodecanucleotides have been synthesized on a solid polymer support with phosphate triester methods by elongation in the 3'-direction. The elongation can occur by condensing the 3'-phosphodiester with 5'-deblocked dinucleotides or trinucleotides having the 3'-(o-chlorophenyl)phosphoro-p-anisidate moiety by using 1-(mesitylene sulfonyl)-3-nitro-1H-1,2,4-tetrazole as the activating reagent. Ohtsuka et al., "Deoxyribonucleic Acids and Related Compounds. VIII. Solid-Phase Synthesis of Deoxyribooligonucleotides with 3'-Modification by Elongation in the 3'-Direction", Chem. Pharm. Bull., **32**, 85-93 (1984).

When adapted to solid phase synthesis, the phosphate triester method produces acceptable results for short fragments (10-20 bases in length), but not for the longer fragments needed to incorporate a scrambled sequence into a form suitable for insertion into a vector. Triester methods have largely been replaced by the phosphoramidite technique, which provides better performance in the synthesis of long fragments. For example, methods to increase the yield of long sequences prepared by solid phase synthesis have been reported using 3'-phosphoramidite functionalized, protected nucleotide dimers. Kumar et al., "Improvements in Oligodeoxyribonucleotide Synthesis: Methyl N,N-Dialkylphosphoramidite Dimer Units for Solid Support Phosphite Methodology", J. Org. Chem., **49**:25, 4905-4911 (1984).

Due to degeneracy in the DNA code, however, total scrambling of all four nucleotides (adenine, guanine, cytosine and thymine) at each site in a DNA sequence leads to more DNA species than peptide species, with the excess growing geometrically as a function of the length of the scrambled sequence. For a hexapeptide, the 64 million possible combinations of 20 amino acids expands to about 68 billion possible combinations of encoding oligonucleotides. Further, the inadvertent inclusion of stop codons sometimes results in

- 3 -

the formation of truncated peptide sequences, which further complicates the analysis.

Two major approaches have been described to overcome this redundancy problem. In a first approach, a semi-scrambled  
5 set of nucleotides is used to take advantage of the third-position redundancy in many codon assignments, for example, N-N-(G/C), which symbolizes a trinucleotide having in the first and second positions a random mix of all four nucleosides and, in the third position, a mix of only guanine and cytosine. This  
10 reduces the number of triplets from 64 to 32, while still encoding all 20 amino acids, and has only one stop codon.

However, each of the four nucleotides has a different rate of incorporation onto the tip of the growing oligonucleotide chain, so that the yield of the resulting  
15 triplets can vary as much as five-fold. Accordingly, to obtain a library containing all hexapeptides, the number of clones that must be examined is more than 15,000 times larger than the number indicated by simple combinatorial arithmetic.

In the second approach, individual codons are  
20 sequentially added to an oligonucleotide on a solid support, usually resin beads, which have been divided into separate containers. The contents of the containers are combined before proceeding to the next codon, for which the resin beads holding the growing chains are again separated into individual  
25 containers. This resin splitting approach does, in principle, produce a more nearly ideal final library, but requires a great deal of synthetic effort. Huse, U.S. Patent No. 5,274,563 issued 23 November 1993; and Glaser et al., "Antibody Engineering by Codon-based Mutagenesis in a Filamentous Phage  
30 Vector System", J. of Immun., 149:12, 3903-13 (1992). Specifically, handling problems, such as static electricity, make quantitative physical transfer of the beads difficult, and chemical inhomogeneity in the microscopically settled beads can lead to poor coupling on some of the beads during solid phase  
35 synthesis.

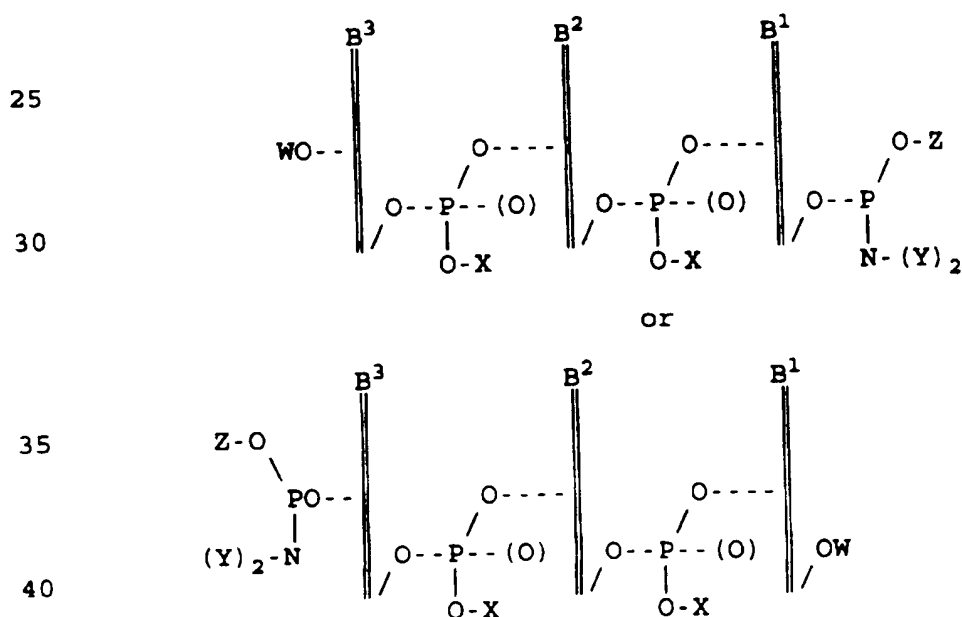
Further, to obtain reasonably uniform representation of each peptide in a hexapeptide library with this approach, more than 64 million beads must be used to assure that the

random pathway taken by each bead through the different containers does not leave out some sequence by mathematical chance. A 1  $\mu$ M synthesis on controlled pore glass (CPG) beads is typical for synthesis of DNA used in most molecular biology purposes. At this synthesis scale, however, only about 25,000 beads are present, which is too few to represent the entire library. Moreover, even if scale-up is attempted, it is a difficult procedure due to increasingly prohibitive handling problems and the attendant costs.

10 The Huse patent also speculates in passing that oligonucleotides could be synthesized from nucleotide triplets, but quickly discourages the use of this approach, stating that "the cost of synthesis from such triplets far exceeds that of synthesis from individual monomers because triplets are not  
15 commercially available." (See, Huse, column 2, lines 18-29) Unexpectedly, the materials and methods of the invention provide a less labor-intensive procedure than that used in the art and, at the same time, provides increased confidence that all the desired sequences will be available, even on a modest synthetic  
20 scale.

## Disclosure of the Invention

The invention relates to compounds of the formula:





wherein W, Y and Z are each independently hydrogen or a protecting group;

X is  $-\text{CH}_2\text{CH}_2\text{CN}$ ;

$\text{B}^1$ ,  $\text{B}^2$  and  $\text{B}^3$  are each independently a base selected from the group consisting of protected adenine, protected guanine, protected cytosine, protected or unprotected thymine and protected or unprotected uracil; and

$\text{R}$  is the residue of a ribose or deoxyribose.

Further, a method has been found for making these compounds and, further, compounds wherein X may be hydrogen or any suitable protecting group, comprising the steps of:

- a. treating a nucleoside comprising a base, a ribose or deoxyribose residue, and a first protecting group at the 5' position or the 3' position, with a trialkylsilyl halide to produce the corresponding 3'- and 5'-substituted nucleoside;
- b. removing the first protecting group at the 5' or 3' position to produce a 5' or 3' deprotected, 3' or 5'-substituted nucleoside;
- c. coupling the 5' or 3' deprotected 3' or 5' substituted nucleoside with a first nucleoside 3' or 5' phosphoramidite and then oxidizing to form a phosphate triester;
- d. deprotecting at the 5'- and 3'-termini to give the corresponding 3',5'-dihydroxy dinucleoside;
- e. coupling the dihydroxy dinucleoside with a second nucleoside 3' or 5' phosphoramidite and oxidizing to produce the two corresponding 3' or 5' hydroxy trinucleotides;
- f. separating away unwanted products; and
- g. converting the 3'- or 5'-hydroxy trinucleotide to a 3'- or 5' phosphoramidite.

In another embodiment, a panel is made up of from two to twenty of these 3'- or 5'-phosphoramidite trinucleotide codons or their complements, where each codon encodes a different amino acid.

Three processes for synthesizing an oligonucleotide are disclosed. To synthesize an oligonucleotide encoding a

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sequence of "n" pre-determined amino acids, or its complement, the process of the invention comprises the steps of:

- (a) coupling a trinucleotide codon, or its complement, onto a solid support;
- 5 (b) sequentially condensing, through a phosphoramidite linkage, with an immediately preceding codon "n-1" trinucleotide codons or their complements, each codon or its complement corresponding to the next pre-determined amino acid in the sequence; and
- 10 (c) cleaving the oligonucleotide from the solid support.

The automated solid phase supported chemistry used in the invention can include a number of materials generally known to those of ordinary skill in the art. Examples of such useful materials include nucleoside-functionalized CPG, i.e., functionalized with deoxyribose cytosine (dC) or another nucleoside, e.g., dG, dU or rC; tetrazole activator solution; acetylating capping solutions; iodine oxidation solutions; 20 dichloroacetic acid deprotecting solvent; and automated DNA synthesizers.

To synthesize an oligonucleotide encoding a peptide having at least one pre-determined amino acid position and at least one random amino acid position, a second synthetic process 25 of the invention comprises the steps of:

- (a) coupling a first trinucleotide codon, or the complement to said codon, onto a nucleoside- or nucleotide-bearing solid support;
- (b) for each pre-determined amino acid position, 30 sequentially coupling through a phosphoramidite to an immediately preceding codon, or complement, a trinucleotide codon, or its complement, corresponding to the pre-determined amino acid;
- (c) for each random amino acid position, coupling to 35 an immediately preceding codon or complement, a mixture of from two to twenty trinucleotide codons, at least two of the trinucleotides